aureus isolated from Tehran hospitals as a rapid and reliable method.

Methods: We studied 585 isolates of different species of *staphylococcus* spp. recovered from patients hospitalized at the 3 Clinical centers in Tehran from October 2005 to October 2007. Antibiotic susceptibility test of isolates was done with 13 antibiotics according to the recommendations of CLSI. The MIC was also done by broth micro dilution assay. The PCR test for *mecA* gene was done.

Results: using biochemical tests 321 (54.7%) isolates were identified as *S. aureus*. 66, 65, 88, 88, 100, 41, 38, 41, 0, 40, 93, 20 and 64% of the *S. aureus* isolates were resistant to kanamycin, cephotaxime, methicillin, oxacillin, ampicillin, erythromycin, clindamycin, sulphamethoxazole-trimethoprime, vancomycin, chloramphenicol, ciprofloxacin, gentamicin and tetracycline respectively. 73% of the isolates were resistant (MIC $\geq$ 256 μg/ml) and 14% were intermediately resistant to methicillin. 100% of MRSA and 63% of intermediate isolates carried *mecA* gene.

Conclusion: In contrast to other studies in Iran the prevalence of Methicillin resistance is rising up in Tehran and most of MRSA isolates were resistance to 5 antibiotics at least. Vancomycin, chloramphenicol, gentamicin and clindamycin are the most effective antibiotics. All of the MRSA isolates had *mecA* gene, and can say this gene is present in both low and high MIC isolates with different expression. Isolates that were intermediate to methicillin but carry *mecA* gene were heteroresistant with high importance. In spite of the other reports in Iran, non of the isolates were resistant to vancomycin. Detection of *mecA* gene is a rapid and reliable method for identification of MRSA isolates.

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44.040

Evaluation of Tigecycline and Other Antimicrobials in Latin America Against Multi-drug Resistant (MDR) Staphylococcus aureus

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Objectives: The emergence of MDR *S. aureus* in Latin America has highlighted the need for surveillance and the continued documentation of the efficacy of existing and new antimicrobials. The Tigecycline Evaluation Surveillance Trial (T.E.S.T.) evaluated the activity of tigecycline and comparators to MDR *S. aureus*(including MR + MS strains) isolated in Latin America.

Methods: 10 hospital sites in 6 countries, between 2004 and 2007, collected 367 clinically significant *S. aureus*. MICs were determined at each site using broth microdilution panels and results interpreted as specified by CLSI at each site.

Results: MIC_{90} of tigecycline and comparators to MDR groups 0—5 are shown in the table below.

Conclusions: Tigecycline in comparison to 10 relevant comparators exhibited the lowest $MIC_{90}$to *S. aureus* isolated in Latin America irrespective of MDR phenotype and multiple drug class resistance.

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44.041

Antibiotic Susceptibility Patterns and Detection of Coa and MecA Genes in the Iranian Isolates of *Staphylococcus aureus*

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Background: Nosocomial infections caused by *Staphylococcus aureus* especially methicillin- resistant *Staphylococcus aureus* (MRSA) belong to the most important multiresistant pathogens worldwide. Therefore, genotypic surveillance of these strains in patients with staphylococcal infections is crucial in control of Nosocomial Infections. The aim of this study was determination of antibiotic susceptibility patterns and detection of coa and mecA genes of the Iranian isolates of *Staphylococcus aureus*.

Methods: In this survey, 65 isolates of *Staphylococcus aureus* were collected from Tehran University hospitals. Antibiotic susceptibility patterns of the all isolates were determined to the 12 antibiotics (methicilin, oxacillin, vancomycin, chloramphenicol, rifampin, tobramycin, gentamicin, ceftriaxone, ciprofloxacin, tetracycline, cotrimoxazole and clindamycin) by the standard disk-diffusion method. According to the genome sequence of the standard strains of *S. aureus*, col and 8325/4, two pairs of primers were designed for coa, and mecA genes.

Results: Thirty three isolates (50.8%) were resistant to methicillin and oxacillin. All the isolates were susceptible to vancomycin, and chloramphenicol. Sixty isolates (92.3%) were sensitive to rifampin. The studied isolates showed different susceptibility patterns to the other antibiotics. The PCR results showed all the isolates (100%) were positive for coa gene. Seven patterns (C1—C7) of coa gene were detected with C1 being the most prevalent; 38 (58.46%). Ten (15.38%), 6(9.23%), 3 (4.61%), 3 (4.61%), 3 (4.61%), and 2 (3.1%) isolates displayed patterns C2, C3, C4, C5, C6 and C7 respectively. The mecA gene was detected in all the methicillin resistant isolates.

Conclusion: The results of the present study showed high rate of methicillin resistance among Iranian isolates of *S. aureus*. The examined isolates showed high variation of the coa gene according to the PCR results. Therefore, continuous surveillance on resistance patterns and characterization of *S. aureus* is highly recommended to control the community and hospital acquired infections caused by this bacterium.

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